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caccagctca	ccgtcttca	ttgccatac				5670

<210> 15
 <211> 238
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> LacZ(/chitobiase Fusion

 <220>
 <221> CDS
 <222> (119)...(238)

<221> -35_signal
<222> (44)...(50)
<223> Lac promoter

<221> -10_signal
<222> (69)...(74)
<223> Lac promoter
<221> protein_bind
<222> (81)...(107)
<223> Lac repressor binding site

<221> protein_bind
<222> (7)...(34)
<223> CAP-cAMP binding site

<400> 15

gcatgcatta atgtgagttt gctcactcat taggcacccc aggcttaca ctttatgctt 60
ccggctcgta tgggtgtgg aattgtgagc ggataacaat ttcacacagg aaacagct 118
atg acc atg att acg cca agc ttg cat gcc tgc agg tcg act cta gag 166
Met Thr Met Ile Thr Pro Ser Leu His Ala Cys Arg Ser Thr Leu Glu
1 5 10 15

gat ccc cgg gta ccg agc tct gag caa caa gtt gta aac tca ctg gct 214
Asp Pro Arg Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala
20 25 30

gat aac ctt gat atc caa tat gaa 238
Asp Asn Leu Asp Ile Gln Tyr Glu
35 40

<210> 16
<211> 40
<212> PRT
<213> Artificial Sequence
<220>
<223> LacZ(/chitobiase Fusion

<400> 16

Met Thr Met Ile Thr Pro Ser Leu His Ala Cys Arg Ser Thr Leu Glu
1 5 10 15
Asp Pro Arg Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala
20 25 30
Asp Asn Leu Asp Ile Gln Tyr Glu
35 40

<210> 17
<211> 22
<212> PRT
<213> Artificial Sequence
<220>
<223> dnaA/chitobiase Fusion

<400> 17

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
1 5 10 15
Leu Val Pro Ser Ser Glu

<210> 18
 <211> 2643
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(2643)

<223> dnaA/Chitobiase Fusion

<400> 18

gtg tca ctt tcg ctt tgg cag cag tgt ctt gcc cga ttg cag gat gag 48
 Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
 1 5 10 15

ttg gta ccg agc tct gag caa caa gtt gta aac tca ctg gct gat aac 96
 Leu Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala Asp Asn
 20 25 30

ctt gat atc caa tat gaa gtg tta act aac cat ggt gct aac gaa ggt 144
 Leu Asp Ile Gln Tyr Glu Val Leu Thr Asn His Gly Ala Asn Glu Gly
 35 40 45

ctt gcg tgc caa gat atg ggc gca gaa tgg gct tct tgt aac aaa gta 192
 Leu Ala Cys Gln Asp Met Gly Ala Glu Trp Ala Ser Cys Asn Lys Val
 50 55 60

aac atg acg ctt gtt aac caa ggt gaa gct gtt gac tca aaa gat tgg 240
 Asn Met Thr Leu Val Asn Gln Gly Glu Ala Val Asp Ser Lys Asp Trp
 65 70 75 80

gct att tac ttc cac agc att cgt ctg att ctg gat gtt gac aac gag 288
 Ala Ile Tyr Phe His Ser Ile Arg Leu Ile Leu Asp Val Asp Asn Glu
 85 90 95

cag ttc aaa atc tct cgt gta acg ggt gac cta cat aag cta gaa cca 336
 Gln Phe Lys Ile Ser Arg Val Thr Gly Asp Leu His Lys Leu Glu Pro
 100 105 110

aca gat aag ttt gac ggc ttc gct gcc ggt gaa gag gtt gtt ctt cca 384
 Thr Asp Lys Phe Asp Gly Phe Ala Ala Gly Glu Val Val Leu Pro
 115 120 125

ttg gtt ggt gaa tac tgg caa cta ttt gaa act gac ttc atg ccg ggt 432
 Leu Val Gly Glu Tyr Trp Gln Leu Phe Glu Thr Asp Phe Met Pro Gly
 130 135 140

gca ttc gtt tct gct cca aac gca gaa cct aag atg att gct tct cta 480
 Ala Phe Val Ser Ala Pro Asn Ala Glu Pro Lys Met Ile Ala Ser Leu
 145 150 155 160

aat act gaa gat gtt gcg tct ttt gtg acg ggt ctt gaa ggt aac aac 528
 Asn Thr Glu Asp Val Ala Ser Phe Val Thr Gly Leu Glu Gly Asn Asn
 165 170 175

cta aaa cgt aca cca gat gac aac aat gta ttt gca aac gct gtg tct	576		
Leu Lys Arg Thr Pro Asp Asp Asn Asn Val Phe Ala Asn Ala Val Ser			
180	185	190	
cgt ttt gag aaa aac gaa gac cta gca aca caa gac gta tca acc acg	624		
Arg Phe Glu Lys Asn Glu Asp Leu Ala Thr Gln Asp Val Ser Thr Thr			
195	200	205	
tta cta cca aca cca atg cac gtt gaa gcg ggt aaa ggc aaa gta gat	672		
Leu Leu Pro Thr Pro Met His Val Glu Ala Gly Lys Gly Lys Val Asp			
210	215	220	
atc gcg gat ggt att gcg ctg cct aaa gac gca ttc gat gcg act cag	720		
Ile Ala Asp Gly Ile Ala Leu Pro Lys Asp Ala Phe Asp Ala Thr Gln			
225	230	235	240
ttc gca gcg att caa gat cgt gca gaa gtt gta ggt gtt gac gtt cgt	768		
Phe Ala Ala Ile Gln Asp Arg Ala Glu Val Val Gly Val Asp Val Arg			
245	250	255	
ggt gat ctt cct gta agc atc act gtt gtt cct gca gac ttc acc ggt	816		
Gly Asp Leu Pro Val Ser Ile Thr Val Val Pro Ala Asp Phe Thr Gly			
260	265	270	
gaa tta gca aaa tct ggt gct tac gaa atg agc atc aaa ggc gac ggt	864		
Glu Leu Ala Lys Ser Gly Ala Tyr Glu Met Ser Ile Lys Gly Asp Gly			
275	280	285	
att gtg att aaa gcg ttc gac caa gca ggc gct ttc tac gca gta caa	912		
Ile Val Ile Lys Ala Phe Asp Gln Ala Gly Ala Phe Tyr Ala Val Gln			
290	295	300	
tct atc ttt ggc ctg gta gat agc caa aat gct gat tct cta cca caa	960		
Ser Ile Phe Gly Leu Val Asp Ser Gln Asn Ala Asp Ser Leu Pro Gln			
305	310	315	320
ctg tct att aaa gat gcg cct cgt ttt gat tac cgt ggt gtg atg gtg	1008		
Leu Ser Ile Lys Asp Ala Pro Arg Phe Asp Tyr Arg Gly Val Met Val			
325	330	335	
gat gtg gct cgt aac ttc cac tct aag gac gca atc ctt gca acg cta	1056		
Asp Val Ala Arg Asn Phe His Ser Lys Asp Ala Ile Leu Ala Thr Leu			
340	345	350	
gac caa atg gca gcg tac aag atg aac aaa ctt cac ctt cac cta acc	1104		
Asp Gln Met Ala Ala Tyr Lys Met Asn Lys Leu His Leu His Leu Thr			
355	360	365	
gat gat gaa ggc tgg cgt tta gaa atc ccg ggt ctg cct gag ctg aca	1152		
Asp Asp Glu Gly Trp Arg Leu Glu Ile Pro Gly Leu Pro Glu Leu Thr			
370	375	380	
gaa gtg ggt gct aac cgt tgt ttc gat aca caa gag aaa agc tgt tta	1200		
Glu Val Gly Ala Asn Arg Cys Phe Asp Thr Gln Glu Lys Ser Cys Leu			
385	390	395	400

ctg cct cag ctt ggc tct ggt cca acg aca gac aac ttt ggc tct ggc Leu Pro Gln Leu Gly Ser Gly Pro Thr Thr Asp Asn Phe Gly Ser Gly 405 410 415	1248
tac ttc agc aaa gca gac tac gtg gaa atc ttg aaa tac gct gaa gca Tyr Phe Ser Lys Ala Asp Tyr Val Glu Ile Leu Lys Tyr Ala Lys Ala 420 425 430	1296
cgt aac att gaa gtg att cca gaa atc gat atg cca gct cac gct cgt Arg Asn Ile Glu Val Ile Pro Glu Ile Asp Met Pro Ala His Ala Arg 435 440 445	1344
gca gca gta gta tca atg gaa gct cgt tac gac cgc cta atg gaa gaa Ala Ala Val Val Ser Met Glu Ala Arg Tyr Asp Arg Leu Met Glu Glu 450 455 460	1392
ggt aaa gaa gct gaa gcg aac gaa tac cgt ctg atg gat cct caa gat Gly Lys Glu Ala Glu Ala Asn Glu Tyr Arg Leu Met Asp Pro Gln Asp 465 470 475 480	1440
aca tca aac gta acg acg gtt cag ttc tac aat aag caa agc ttc atc Thr Ser Asn Val Thr Val Gln Phe Tyr Asn Lys Gln Ser Phe Ile 485 490 495	1488
aac cca tgt atg gaa tct tca act cgc ttt gtt gat aag gtg att tca Asn Pro Cys Met Glu Ser Ser Thr Arg Phe Val Asp Lys Val Ile Ser 500 505 510	1536
gaa gtg gca gca atg cac caa gaa gct ggc gct cca cta aca act tgg Glu Val Ala Ala Met His Gln Glu Ala Gly Ala Pro Leu Thr Thr Trp 515 520 525	1584
cac ttc ggt ggt gac gaa gcg aag aac atc aag cta ggt gct ggt ttc His Phe Gly Gly Asp Glu Ala Lys Asn Ile Lys Leu Gly Ala Gly Phe 530 535 540	1632
caa gac gtt aac gca gaa gat aaa gta agc tgg aaa ggc acg att gac Gln Asp Val Asn Ala Glu Asp Lys Val Ser Trp Lys Gly Thr Ile Asp 545 550 555 560	1680
ctg tct aaa caa gac aag ccg ttt gca cag tct cca caa tgt cag acg Leu Ser Lys Gln Asp Lys Pro Phe Ala Gln Ser Pro Gln Cys Gln Thr 565 570 575	1728
cta atc aca gat ggc aca gtc agt gac ttt gct cac cta cca agc cac Leu Ile Thr Asp Gly Thr Val Ser Asp Phe Ala His Leu Pro Ser His 580 585 590	1776
ttc gcg gaa gaa gtg tcg aag att gtt gct gag aaa ggc att cca aac Phe Ala Glu Glu Val Ser Lys Ile Val Ala Glu Lys Gly Ile Pro Asn 595 600 605	1824
ttc caa gct tgg caa gat ggt ttg aaa tac agt gac ggc gaa aaa gcg Phe Gln Ala Trp Gln Asp Gly Leu Lys Tyr Ser Asp Gly Glu Lys Ala 610 615 620	1872
ttc gct aca gaa aat act cgc gta aac ttc tgg gac gtt ctg tac tgg	1920

Phe Ala Thr Glu Asn Thr Arg Val Asn Phe Trp Asp Val Leu Tyr Trp	625	630	635	640	
ggc ggt act tcc tca gtg tac gag tgg tct aag aaa ggt tac gac gtc					1968
Gly Gly Thr Ser Ser Val Tyr Glu Trp Ser Lys Lys Gly Tyr Asp Val					
645	650	655			
att gtt tct aac cca gat tac gtg tac atg gat atg cca tac gaa gtt					2016
Ile Val Ser Asn Pro Asp Tyr Val Tyr Met Asp Met Pro Tyr Glu Val					
660	665	670			
gac ccg aaa gag cgt ggt tac tac tgg gca aca cgt gca acg gat act					2064
Asp Pro Lys Glu Arg Gly Tyr Trp Ala Thr Arg Ala Thr Asp Thr					
675	680	685			
cgt aag atg ttt ggc ttt gca cca gag aac atg cct caa aac gca gaa					2112
Arg Lys Met Phe Gly Phe Ala Pro Glu Asn Met Pro Gln Asn Ala Glu					
690	695	700			
act tct gta gat cgc gat ggc aat ggc ttt act ggt aaa ggt gaa atc					2160
Thr Ser Val Asp Arg Asp Gly Asn Gly Phe Thr Gly Lys Gly Glu Ile					
705	710	715	720		
gaa gcg aaa cct ttc tac ggt cta tct gca caa ctt tgg tct gag aca					2208
Glu Ala Lys Pro Phe Tyr Gly Leu Ser Ala Gln Leu Trp Ser Glu Thr					
725	730	735			
gta cgt aac gac gag caa tac gag tac atg gta ttc cct cgc gtc ctc					2256
Val Arg Asn Asp Glu Gln Tyr Glu Tyr Met Val Phe Pro Arg Val Leu					
740	745	750			
gct gct gct cag cgt gca tgg cac cgt gct gac tgg gaa aac gac tac					2304
Ala Ala Ala Gln Arg Ala Trp His Arg Ala Asp Trp Glu Asn Asp Tyr					
755	760	765			
aaa gtt ggt gtt gag tac tcg caa aac tct aat cta gtt gat aaa gca					2352
Lys Val Gly Val Glu Tyr Ser Gln Asn Ser Asn Leu Val Asp Lys Ala					
770	775	780			
tcg cta aac caa gac tac aac cgc ttt gcg aac gta ctt ggt caa cgt					2400
Ser Leu Asn Gln Asp Tyr Asn Arg Phe Ala Asn Val Leu Gly Gln Arg					
785	790	795	800		
gaa ctg gct aag cta gaa aaa tca ggt att gac tac cgc cta cca gta					2448
Glu Leu Ala Lys Leu Glu Lys Ser Gly Ile Asp Tyr Arg Leu Pro Val					
805	810	815			
cca ggt gca aaa gta gaa gat ggt aag cta gca atg aac gtt cag ttc					2496
Pro Gly Ala Lys Val Glu Asp Gly Lys Leu Ala Met Asn Val Gln Phe					
820	825	830			
cct ggc gta acg ctt caa tac tct ctg gat ggt gag aac tgg ttg act					2544
Pro Gly Val Thr Leu Gln Tyr Ser Leu Asp Gly Glu Asn Trp Leu Thr					
835	840	845			
tat gca gac aac gct cgt cca aat gta act ggt gaa gtc ttc atc cgc					2592
Tyr Ala Asp Asn Ala Arg Pro Asn Val Thr Gly Glu Val Phe Ile Arg					

850

855

860

tcg gta tct gct aca ggt gag aag gta agc cgt atc act agc gtg aaa	2640
Ser Val Ser Ala Thr Gly Glu Lys Val Ser Arg Ile Thr Ser Val Lys	
865 870 875 880	

taa	2643
*	

<210> 19
 <211> 880
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> dnaA/Chitobiase Fusion

<400> 19

Met Ser Leu Ser Leu Trp Gln Gln Cys	Leu Ala Arg Leu Gln Asp Glu
1 5 10 15	
Leu Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala Asp Asn	
20 25 30	
Leu Asp Ile Gln Tyr Glu Val Leu Thr Asn His Gly Ala Asn Glu Gly	
35 40 45	
Leu Ala Cys Gln Asp Met Gly Ala Glu Trp Ala Ser Cys Asn Lys Val	
50 55 60	
Asn Met Thr Leu Val Asn Gln Gly Glu Ala Val Asp Ser Lys Asp Trp	
65 70 75 80	
Ala Ile Tyr Phe His Ser Ile Arg Leu Ile Leu Asp Val Asp Asn Glu	
85 90 95	
Gln Phe Lys Ile Ser Arg Val Thr Gly Asp Leu His Lys Leu Glu Pro	
100 105 110	
Thr Asp Lys Phe Asp Gly Phe Ala Ala Gly Glu Val Val Leu Pro	
115 120 125	
Leu Val Gly Glu Tyr Trp Gln Leu Phe Glu Thr Asp Phe Met Pro Gly	
130 135 140	
Ala Phe Val Ser Ala Pro Asn Ala Glu Pro Lys Met Ile Ala Ser Leu	
145 150 155 160	
Asn Thr Glu Asp Val Ala Ser Phe Val Thr Gly Leu Glu Gly Asn Asn	
165 170 175	
Leu Lys Arg Thr Pro Asp Asp Asn Val Phe Ala Asn Ala Val Ser	
180 185 190	
Arg Phe Glu Lys Asn Glu Asp Leu Ala Thr Gln Asp Val Ser Thr Thr	
195 200 205	
Leu Leu Pro Thr Pro Met His Val Glu Ala Gly Lys Gly Lys Val Asp	
210 215 220	
Ile Ala Asp Gly Ile Ala Leu Pro Lys Asp Ala Phe Asp Ala Thr Gln	
225 230 235 240	
Phe Ala Ala Ile Gln Asp Arg Ala Glu Val Val Gly Val Asp Val Arg	
245 250 255	
Gly Asp Leu Pro Val Ser Ile Thr Val Val Pro Ala Asp Phe Thr Gly	
260 265 270	
Glu Leu Ala Lys Ser Gly Ala Tyr Glu Met Ser Ile Lys Gly Asp Gly	
275 280 285	
Ile Val Ile Lys Ala Phe Asp Gln Ala Gly Ala Phe Tyr Ala Val Gln	
290 295 300	
Ser Ile Phe Gly Leu Val Asp Ser Gln Asn Ala Asp Ser Leu Pro Gln	

305	310	315	320
Leu Ser Ile Lys Asp Ala Pro Arg Phe Asp Tyr Arg Gly Val Met Val			
325	330	335	
Asp Val Ala Arg Asn Phe His Ser Lys Asp Ala Ile Leu Ala Thr Leu			
340	345	350	
Asp Gln Met Ala Ala Tyr Lys Met Asn Lys Leu His Leu His Leu Thr			
355	360	365	
Asp Asp Glu Gly Trp Arg Leu Glu Ile Pro Gly Leu Pro Glu Leu Thr			
370	375	380	
Glu Val Gly Ala Asn Arg Cys Phe Asp Thr Gln Glu Lys Ser Cys Leu			
385	390	395	400
Leu Pro Gln Leu Gly Ser Gly Pro Thr Thr Asp Asn Phe Gly Ser Gly			
405	410	415	
Tyr Phe Ser Lys Ala Asp Tyr Val Glu Ile Leu Lys Tyr Ala Lys Ala			
420	425	430	
Arg Asn Ile Glu Val Ile Pro Glu Ile Asp Met Pro Ala His Ala Arg			
435	440	445	
Ala Ala Val Val Ser Met Glu Ala Arg Tyr Asp Arg Leu Met Glu Glu			
450	455	460	
Gly Lys Glu Ala Glu Ala Asn Glu Tyr Arg Leu Met Asp Pro Gln Asp			
465	470	475	480
Thr Ser Asn Val Thr Thr Val Gln Phe Tyr Asn Lys Gln Ser Phe Ile			
485	490	495	
Asn Pro Cys Met Glu Ser Ser Thr Arg Phe Val Asp Lys Val Ile Ser			
500	505	510	
Glu Val Ala Ala Met His Gln Glu Ala Gly Ala Pro Leu Thr Thr Trp			
515	520	525	
His Phe Gly Gly Asp Glu Ala Lys Asn Ile Lys Leu Gly Ala Gly Phe			
530	535	540	
Gln Asp Val Asn Ala Glu Asp Lys Val Ser Trp Lys Gly Thr Ile Asp			
545	550	555	560
Leu Ser Lys Gln Asp Lys Pro Phe Ala Gln Ser Pro Gln Cys Gln Thr			
565	570	575	
Leu Ile Thr Asp Gly Thr Val Ser Asp Phe Ala His Leu Pro Ser His			
580	585	590	
Phe Ala Glu Glu Val Ser Lys Ile Val Ala Glu Lys Gly Ile Pro Asn			
595	600	605	
Phe Gln Ala Trp Gln Asp Gly Leu Lys Tyr Ser Asp Gly Glu Lys Ala			
610	615	620	
Phe Ala Thr Glu Asn Thr Arg Val Asn Phe Trp Asp Val Leu Tyr Trp			
625	630	635	640
Gly Gly Thr Ser Ser Val Tyr Glu Trp Ser Lys Lys Gly Tyr Asp Val			
645	650	655	
Ile Val Ser Asn Pro Asp Tyr Val Tyr Met Asp Met Pro Tyr Glu Val			
660	665	670	
Asp Pro Lys Glu Arg Gly Tyr Tyr Trp Ala Thr Arg Ala Thr Asp Thr			
675	680	685	
Arg Lys Met Phe Gly Phe Ala Pro Glu Asn Met Pro Gln Asn Ala Glu			
690	695	700	
Thr Ser Val Asp Arg Asp Gly Asn Gly Phe Thr Gly Lys Gly Glu Ile			
705	710	715	720
Glu Ala Lys Pro Phe Tyr Gly Leu Ser Ala Gln Leu Trp Ser Glu Thr			
725	730	735	
Val Arg Asn Asp Glu Gln Tyr Glu Tyr Met Val Phe Pro Arg Val Leu			
740	745	750	
Ala Ala Ala Gln Arg Ala Trp His Arg Ala Asp Trp Glu Asn Asp Tyr			
755	760	765	

Lys Val Gly Val Glu Tyr Ser Gln Asn Ser Asn Leu Val Asp Lys Ala
770 775 780
Ser Leu Asn Gln Asp Tyr Asn Arg Phe Ala Asn Val Leu Gly Gln Arg
785 790 795 800
Glu Leu Ala Lys Leu Glu Lys Ser Gly Ile Asp Tyr Arg Leu Pro Val
805 810 815
Pro Gly Ala Lys Val Glu Asp Gly Lys Leu Ala Met Asn Val Gin Phe
820 825 830
Pro Gly Val Thr Leu Gln Tyr Ser Leu Asp Gly Glu Asn Trp Leu Thr
835 840 845
Tyr Ala Asp Asn Ala Arg Pro Asn Val Thr Gly Glu Val Phe Ile Arg
850 855 860
Ser Val Ser Ala Thr Gly Glu Lys Val Ser Arg Ile Thr Ser Val Lys
865 870 875 880

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Concluded